

FIGURE 1

Fucosyltransferase nucleotide sequence from strain 1182 FutB (SEQ ID NO:1)

Protein sequence from strain 1182 FutB (SEQ ID NO:2)

FIGURE 2

Fucosyltransferase from strain 1111 FutA

Nucleotide coding sequence (SEQ ID NO:3)

atgttccaacccctattagatgccttatagaagcgctccattgaaaaaatggccttaatctccccccctaaaatcgctgtgg
cgaattggggagatgaagaaattaaaaattaaaagagcgttatttatcctaagccaggattacaatcttaca
ccgaaacctgataaacctgcggacatgcgtttgttaacccttgatcggcagaaaaatcttacatcaaagcgaaaaa
gggtgtttacccggtaaaatgaagtccctaactcaacctttagtacgccataggcgtttagatgaaattggactttagagatcgt
tatttgagaatgccttgtattatgcattaaagccgagctgttaatgacaccactcgccttataactccaacctgaca
gccttatgcittaaaaaacccctccatatttaagaaaaccaccccaattgtgcgcagtagtgaataatgagagtgatccttig
aaaagagggttgcgagttgtcgaagcaaccctaacgccttagaaggaacgcgtttatgaggcttaacgcgtattgagcc
agttgcgtggggagggagcgtaaaaacactttagcgtataatgtcaaaaacaagagcgcagtttaagccaatacaaattcaat
ctgttttggaaaacactcaaggctatggctatgtactgaaaagatcattgacgcatttcagccataccattcttatttgggg
agtcccagcgtggcgaagatttacccctaagagtttgtaattgtccatgattcaacaactttagatgaaagcgtattgactatata
gatacttgcacacgcacccaaacgcatttttagacatgcactatgaaaaccctttaacactattgtatggaaagcgttacttttacca
aaatttgagttttaaaaaatcttagattttttaaaacgattttagaaaacgcacacgcattatcacgataacccttcatttctatcgt
atttgaafgagcctcagtatctattgtgtttgaggtaattatgtatgatttgaggtaattatgtatgatttgaggtaattatgt
gatttgaggtaattatgtagcgcctttacaaaacgcctcgccttattagaactctcaaaacaccactttaaaatctatcgcaaa
gccttatcaaaaatccttgccttgcgtgcataaggagatgggttaaaaagttaa

Protein sequence (SEQ ID NO:4)

mfqplldafiesaplkkwplnlpplkiavanwwgdeeikkfkksvlyfilsqhytitlhrnpdkpadivfgnplgsarkilsy
qnakrvfytgenepnfnlfdfaigfdeldfrdrylmplyayylhykaelvndtspyklqpdslyalkkpshhfkenhpnlcavvnnesdplkrgfasfvasnpnaprrnafydealnaiepvaggsvkntlgynvknkseflsqykfnlcfentqgygyvt
ekiidayfshtipiywgspsvakdfnpksfvnhdfnnfdeaidyirylhthpnayldmhyenplntidgkayfyqnlfskkildffktilendtiyhdpnfifyrndlnepevsidglrvnyddlrnvnyddlrnvnyerllqnaspallesqnttfkiyrkayqkslplairrwvkk*

FIGURE 3

Strain 1218 *FutB* nucleotide sequence (SEQ ID NO:5)

atgttccaacccctattagacgcitataatagaagcgcttcattgaaaaaaattacctctaaatctcccccccccctaaaatcgcgt
tggcgaattggggggagatgaagaggttgaagaattaaaagaacattcttattttatctcagtcaggcattacacaatcaccc
ccaccaaaaaccccaacgaaccctccatctgtcttggcagtccattggatcagccagaaaaatcttatccatcaaacgcaa
aaagagtgtttacaccggtaaaaacgaatcgcctaattcaacctcttgcatttgcgcatttttagat
cgittatthaagaatgccttatattatgatagactacaccataaagccgagagcgtgaatgacaccacttcgccttacaaactcaa
ctgacagccittatgcittaaaaaacccctccatcatttaagaaaaccaccccaatttatgcgcagtagtgcacaatgagagc
atccttgcaggggttgcgagtttgcgcacccctaaacgccttacaaaaggatgccttgcgcaccccttata
gagccagtttgcgcacccctaaacgccttacaaaaggatgccttgcgcaccccttata
tcaatctgtttgaaaactcacaaggctatggctatgtactaaaaatcattgcgccttgcgcaccccttata
ggggagtttgcgcacccctaaacgccttacaaaaggatgccttgcgcaccccttata
gcgcataacttgcacacgcacccaaacgccttgcgcaccccttacaaaaggatgccttgcgcaccccttata
aaaaatttgcgtttaaaatcctagatttttgcgcaccccttacaaaaggatgccttgcgcaccccttata
gatttgatgcgcgttaatcttgcgcaccccttacaaaaggatgccttgcgcaccccttata
tgatgttgcgcgttaatcttgcgcaccccttacaaaaggatgccttgcgcaccccttata
gggttaatttgcgcaccccttacaaaaggatgccttgcgcaccccttata
acgcctcgccttattagaactctccttacaaaacccactttaaaatctatgcgcaccccttacaaaatccttgcgcaccccttata
cgagaaatgttgcgcgttaatcttgcgcaccccttacaaaaggatgccttgcgcaccccttata

Predicted protein strain 1218 FutB (SEQ ID NO:6)

mfqplldayiesasiekitsksppplkiavanwwgdeeveefknilyfilsqhytitlhqnepSDLVfgspigsarkilsy
qnakrvfytgenespnfnlfdfaigfdeldfrdrylmplyydrlhkaesvndtspyklkpdslyalkkpshhfkenhpnl
cavvnnesdplkrkgfasfvasnnpaprnatydalnsiepviggsvkntlgyniknkseflsqykfnlcfcensqgygyvte
kiidayfshtipiwygspsvaqdfnpksfvnvcdfkdfdeaidhvrylhthpnayldmlyenplntldgkayfyqnlfsfkki
ldffktilendtiyhdnpfifyrdlneplisiddlrnyddlrnyddlrnyddlrnyddlrnyddlrnyddlrnyddlr
vnyddlrvcddlrnyddlrnyerllqnaspllelsqntfkirkyakqksplllaarklikklgl*

FIGURE 4

Fucosyltransferase strain 19C2 FutB nucleotide sequence (SEQ ID NO:7)

atgttccaacccatttagacgcttatagacagcaccgttagatgaaaccgattataagccccattaaatatgccttagcg
aattggcgccttgataaaagagaagcaaagggttagaaaaaaattatcttacatttcatttaagtcagcattacacaatcg
tctccaccgaaacctgataaacctcgacatcggtttggtaaccccttggatcagccagaaaaatcctatcctatcaaacg
ctaaaagggtttacaccggtaaaaacgaagtccctaattcaaccttgcattacgccataggcttgcattttgactttaga
gatcggtttttgagaatgccttatattatgatagactacaccataaagccgagagcgtgaatgacaccaccgcacccataaagatt
aaatctgacagcccttatgcctttaaaagccctccatcatttaaagaaaaccacccacattatgcgcgctaatcaataatgaga
tcgatcccttggaaaagagggttgcgagcttgcgaagcaaccctaacgccttataaggAACGCTTCTATGAGGCTTAAATT
tattgagccagttactggggagggagcgtgagaaacactttaggtataacgtcaaaaacaaaacgaattttgcacccatc
aattcaatctgtgccttggaaaacactcaaggctatggctatgttactgaaaaatcattgacgcctacttcagccacaccattcstat
ttattggggggagtcctagcgtggcggaaagatttaacccc

Strain 19C2 FutB protein sequence (SEQ ID NO:8)

mfqpIldayidstrldetdykpplnialanwwpldkreskgfrkkfilhfilsqhytialhrnpdkpadivfgnplgsarkilsy
qnakrvfytgenepnfnlfdfaigfdeldfrdrylrmplyydrlhkaesvndtapykiksdslyalkkpshhfkhenhph
lcalinneidplkrgfasfvasnnapirnafyealnsiepvtggsvrntlgyvnknkneflsqykfnlcfcntqgygyvtek
iidayshtipiywggvpsvakdfnp

FIGURE 5

Strain 915 FutA fucosyltransferase nucleotide coding sequence (SEQ ID NO:9)

atggcctaaatctccccccctaaaaatcgctgtggcgaattggtggggagatgaagaaaattaaaaagagcgttctttatttatctaagccaggcattacacaatcacttacaccgaaacctgataaacctgcggacatcgtcttgtaaccccttggatcagccagaaaaatcttatcctatcaaaacgcaaaaagggtgtttacaccggtaaaaatgaagtccctaactcaaccctttgattacgccataggctt

Protein sequence from Strain 915 FutA (SEQ ID NO:10)

maskspplkiavanwwgdeeikkfkksvlyfilsqhytitlhrnpdkpadivfgnplgsarkilsyqnakrvfytnenevpnfnlfdfaigf

FIGURE 6

Strain 26695 FutA fucosyltransferase nucleotide coding sequence (SEQ ID NO:11)

atgttccaacccctattagacgccttatagaaagcgttcattgaaaaaatggccttaaatccccccccccctaaaatc
gctgtggcaattgggggagatgaagaattaagaattaaaagagcgttcttattttatcctaagccaacgc
accctccaccaaaccctaatttcagatctagtttagcaatcctcttggagccggctagaaagattttatc
taaacgagtgtttacaccggtaaaaacgaatcacctaattcaacctcttattttatc
tcgttatttgagaatgccttgtattatgccttgcactataaagccgagcttgttaatg
acaacagccttatgccttaaaaaaccctctcatcatttaagaaaaccacc
aictttaaaagagggttgcagttttagcgagcaacgc
taacgc
tccata
gagccagttactgggggaggaagtgtgagaaacactttag
gtataaggttggaaacaaaagcgagtttaagcc
aatacgt
tcaatctctgtttgaaaactcgc
aagggttatggctatgt
taacc
gaaaaatc
ttgatgc
gtattttag
ccatacc
atttatt
ggggag
tccc
cagc
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gt
aa

Protein coding sequence Strain 26695 FutA (SEQ ID NO:12)

mfqplldafiesasiekmaskssppplkiavanwwgdeeikefkksvlyfilsqryaitlhqnepnfsdlvfnplgaarkil
syqntkrfvytgenespnfnlfdfaigfdelfndrylmplyyahhykaelvndttapyklkdnslyalkkpkshfkenh
pnlcavvndesdllkrgfasfasnanapmrnafydalnsiepvttggsvrntlgykvgnkseflsqykfnlcensqgygy
vtekildayfshtipiwygspsvakdfnpksfvnhdfnnfdeaidyikylhthpnayldmilyenplntldgkayfyqdlsf
kkildffktilendtiyhkfstsfnweydlhkplvsiddrvnyddlrnvnydrlqnaspllelsqnttfkiyrkayqksplllrav
rklvkkgl*

FIGURE 7

19C2A fucosyltransferase nucleotide sequence (SEQ ID NO:13)

atgttccaacccttactagacgccttatagaaagtgctccaatt

19C2A predicted protein sequence (SEQ ID NO:14)

mfqpplldafiesapi

FIGURE 8

Protein sequence from strain 1182 FutB aligned with pfam00852, Glyco_transf_10, Glycosyltransferase family 10

Query:	23	PPPLKIAVANWWGDEEVEEFKKNILYFILSQHYTITLHQNPNEPSDLVFGS-PIGSARKI	81
Sbjct:	11	TVPLLAIYTWWSLIEYKEWKSPIYFIGSQAPQPPLR---ILLWTWPNGNPLALSDCP	67
Query:	82	LSYQNAKRVFYTGEN---ESPNFNLF---DYAIGFDELDFRDRYLRLMPYYDRLHHKAES	135
Sbjct:	68	LSYQNTARCRLTANRSPLESADAVLFHHRDLSKGFPDLPPSPRPGQPWVWASMESPNS	127
Query:	136	-VNDTTSPYKLKPDSLALKKPSHHFKENHPNLCAVVNNESDPLKRGFASFVASNPN-AP	193
Sbjct:	128	GLNDLRDGYNWTLSYRADSDAFHPYGYLEPRLSQVVAAPLLSAKRKGAAWVSNCNTRS	187
Query:	194	KRNAFYDVLSIEPVIGGGSVKNTLGYNIKNKSEFLSQYKFNLCFENSQGYGYVTEKIID	253
Sbjct:	188	KRERFYKQLNKHLQVDVGGRVANPLPLKVGCLVETLSQYKFYLAFENSQHYDYVTEKLWK	247
Query:	254	-AYFSHTIPIYWGPSVAQDFNP-KSFVNVCDFKDFDEAIDHVRYLHTHPNAYL	305
Sbjct:	248	NALQAGTIKVVLGPRAVYEDFVPPKSFIHVDDFKSPKEIADYLLYLDTNPTAYS	301

FIGURE 9

Fucosyltransferase from strain 1111 FutA aligned with pfam00852, Glyco_transf_10, Glycosyltransferase family 10

Query:	27	IAVANWWGDEEIKKFKKSVLYFILSQHYTITLHRNPDKPADIYFG-NPLGSARKILSYQN	85
Sbjct:	16	LAIYTWWSLIEYKEWKKSPIYFIGSQAPQPPLR---ILLWTWFNGNPLALSDCPLSYQN	72
Query:	86	AKRVFYTGEN---EVPNFNLF---DYAIGFDDELFRDRYLRLMPLYYAYLHYKAEL-VNDT	138
Sbjct:	73	TARCRLTANRSPLESADAVLFHHRDLSKGFPDLPPSPRPPGQPWVWASMESPSNSGLNDL	132
Query:	139	TSPYKLQPDLSYALKKPSSHFKENHPNLCAVVNNESDPLKRGFASFVASNPNA-APRRNAF	197
Sbjct:	133	RDGYFNWTLTSYRADSDAFHPYGYLEPRLSQVVAAPLLSAKRKGAAWVVSNCNTRSKRERF	192
Query:	198	YEALNAIEPVAGGGSVKNTLGYNVNKNKSEFLSQYKFNLCFENTQGYGYVTEKIID-AYFS	256
Sbjct:	193	YKQLNKHLQVDVGGRVANPLPLKVGCLVETLSQYKFYLAFENSQHYDYVTEKLWKNALQA	252
Query:	257	HTIPIYWGPSPSVAKDFNPKS-FVNVHDFNNFDEAIDYIRYLHHTHPNAYLDMHYENPLNTI	315
Sbjct:	253	GTIPVVLGPRAVYEDFVPPKSFIHVDDFKSPKEIADYLLYLDTNPTAYS-----	301
Query:	316	DGKAYFYQNLSFKKILDFFKTILENDTIYHDNPFIYRDLNEPSVSIDGLRVNYDDL RVN	375
Sbjct:	302	-----EYFEWRYDLRVRLFSDALR-----	321
Query:	376	YDDLRLVNYDDLRLVNYERLLQNAPSLPLELSQNTTFKIYRKAYQ	417
Sbjct:	322	-----YDEGFCRVCRVLLQNAPD-----RYKTYPNIAKWFQ	351

FIGURE 10

Protein sequence from strain 1218 FutB aligned with pfam00852, Glyco_transf_10, Glycosyltransferase family 10

Query:	23	PPPLKIAVANWWGDEEVEFKKNILYFILSQHYTITLHQNPNEPSDLVFGS-PIGSARKI	81
Sbjct:	11	TVPLLAIYTWWSLIEYKEWKSPIYFIGSQAPQPPLR--ILLWTWPFGNPLALSDCP	67
Query:	82	LSYQNAKRVFYTGEN---ESPNFLF---DYAIGFDELDFRDRYLRMPLYYDRLHHKAES	135
Sbjct:	68	LSYQNTARCRLTANRSPLESADAVLFHHRDLSKGFPDLPPSPRPGQPVWASMESPSNS	127
Query:	136	-VNDTTSPYKLKPDSLYALKPSSHFKENHPNLCAVVNNESDPLKRGFASFVASNPN-AP	193
Sbjct:	128	GLNDLRLGYFNWTLSYRADSDAFHPYGYLEPRLSQVNVNAPLLSAKRKGAAWVVSNCNTRS	187
Query:	194	KRNAFYDALNSIEPVIGGGSVKNTLGYNIKNKSEFLSQYKFNLCFENSQGYGYVTEKIID	253
Sbjct:	188	KRERFYKQLNKHLQVDVGGRVANPLPLKVGCIVETLSQYKFYLAFENSQHYDYVTEKLWK	247
Query:	254	-AYFSHTIPIYWGSPSVAQDFNP-KSFVNVCDFKDFDEAIDHVRYLHTHPNAYLDMLYEN	311
Sbjct:	248	NALQAGTIKVVLGPRAVYEDFVPPKSFIHVDDFKSPKELADYLLYLDTNPTAYS-----	301
Query:	312	PLNTLDGKAYFYQNLNSFKKILDFFKTILENDTIYHDNPFIFYRDLNEPLISIDDLRVNYD	371
Sbjct:	302	-----EYFEWRYDLRVRLFSWDALR--YD	323
Query:	372	DLRVNYDDLRLRVNYDDLRLRVNYDDLRLRVNYD	399
Sbjct:	324	EGFCRVCRLLQNAPDRYKTYPNIAKWFQ	351

FIGURE 11

Protein sequence from strain 19C2 FutB aligned with pfam00852, Glyco_transf_10, Glycosyltransferase family 10

Query:	22	PPLNIALANWWPLDKRESKGFRKKFILHFILSQHYTIALHRNPDKPADIVFG-NPLGSAR	80
Sbjct:	12	VPLLLAIYTWWSL--IEYKEW-KKSPIYFIGSQAPQPPLR---ILLWTWPFGNPLALSD	65
Query:	81	KILSYQNAKRVFYTGEN---EVPNFNLF---DVAIGFDELDFRDRYLRMPLYYDRLHHKA	134
Sbjct:	66	CPLSYQNTARCRLLTANRSPLESADAVLFHHRDLSKGFPDLPSPRPPGQPWWASMESPS	125
Query:	135	ES-VNDTTAPYKIKSDSLYALKPSSHFKENPHLCALINNEIDPLKRGFASFVASNP-	192
Sbjct:	126	NSGLNDLRLDGYFNWTLSYRADSDAFHPYGYLEPRLSQVNVNAPLLSAKRKGAAWVVSNCNT	185
Query:	193	APIRNAFYEALNSIEPVTVGGGSVRNLTGYNVKNKNEFLSQYKFNLCFENTQGYGYVTEKI	252
Sbjct:	186	RSKRERFYKQLNKHQLQDVGGRVANPLPLKVGCLVETLSQYKFYLAFENSQHYDYVTEKL	245
Query:	253	ID-AYFSHTIPIYWGGVPSVAKDFNP	277
Sbjct:	246	WKNALQAGTIPVVVLGP-RAVYEDFVP	270

FIGURE 12

	1	50
1111FutA.pep	(1) MFQPLLLDA E IESAP I KKWPLN--LPPLKIAVANWWGDEE I KK---FKKS V	
19C2A.pep	(1) MFQPLLLDA E IESAP I --	
915A.pepneose	(1) -----MASK-SPPLKIAVANWWGDEE I KK---FKKS V	
26695A.pep	(1) MFQPLLLDA E IESAS I EKMA S KSPPPLKIAVANWWGDEE I KE---FKKS V	
1182B.pep	(1) MFQPLLLDA E IESAS I EKIT S KS-PPPLKIAVANWWGDEE I EE---FKKN I	
1218B.pep	(1) MFQPLLLDA E IESAS I EKIT S KS-PPPLKIAVANWWGDEE I EE---FKKN I	
ORF19C2B.pep	(1) MFQPLLLDA E ISTRE D ETDYK---PPLNT A ANWWPLDKRESKGFRKKF I	
Consensus	(1) MFQPLLLDAFIESA IEK SK PPLKIAVANWWGDEEI FKK I	
	51	100
1111FutA.pep	(46) LYFILSQHYTITLHRNPDKPA D IVFGNPLGSARKILSYQNAKRVFY T GEN	
19C2A.pep	(16) -----	
915A.pepneose	(29) LYFILSQHYTITLHRNPDKPA D IVFGNPLGSARKILSYQNAKRVFY T GEN	
26695A.pep	(48) LYFILSORYAITLHQNPNEF D IVFSNPLGSARKILSYQNTKRVFY T GEN	
1182B.pep	(47) LYFILSQHYTITLHQNPNEPSD D IVFGSP I GSARKILSYQNAKRVFY T GEN	
1218B.pep	(47) LYFILSQHYTITLHQNPNEPSD D IVFGSP I GSARKILSYQNAKRVFY T GEN	
ORF19C2B.pep	(48) LYFILSQHYTITLHQNPDKPA D IVFGNPLGSARKILSYQNAKRVFY T GEN	
Consensus	(51) LYFILSQHYTITLH NP PADIVFGNPLGSARKILSYQNAKRVFY T GEN	
	101	150
1111FutA.pep	(96) EVPNFNLFDYAI G DELD F RDRYL R MPLY YAYL H M KAE L VNDTTSPYKLQ	
19C2A.pep	(16) -----	
915A.pepneose	(79) EVPNFNLFDYAI G DELD F RDRYL R MPLY YAYL H M KAE L VNDTTSPYKLQ	
26695A.pep	(98) ESPNFNLFDYAI G DELD F RDRYL R MPLY YAYL H M KAE L VNDTTSPYKLK	
1182B.pep	(97) ESPNFNLFDYAI G DELD F RDRYL R MPLY YAYL H M KAE S VNDTTSPYKLK	
1218B.pep	(97) ESPNFNLFDYAI G DELD F RDRYL R MPLY YAYL H M KAE S VNDTTSPYKLK	
ORF19C2B.pep	(98) EVPNFNLFDYAI G DELD F RDRYL R MPLY YAYL H M KAE S VNDTTSPYKLK	
Consensus	(101) E PN F NLF D YAI G DELD F RDRYL R MPLY YAYL H M KAE S VNDTTSPYKLK	
	151	200
1111FutA.pep	(146) PDSIYALKKPSHHEKENHPNLCAVVNNESDPLIKRGFASFVASNPNA P RRN	
19C2A.pep	(16) -----	
915A.pepneose	(93) -----	
26695A.pep	(148) DNSIYALKKPSHHEKENHPNLCAVVNNESDPLIKRGFASFVASNPNA P MRN	
1182B.pep	(147) PDSIYALKKPSHHEKENHPNLCAVVNNESDPLIKRGFASFVASNPNA P KRN	
1218B.pep	(147) PDSIYALKKPSHHEKENHPNLCAVVNNESDPLIKRGFASFVASNPNA P KRN	
ORF19C2B.pep	(148) SDSIYALKKPSHHEKENPHLCAVVNNESDPLIKRGFASFVASNPNA P IRN	
Consensus	(151) D S LYALKKPSHHFKENHPNLCAVVNNESDPLIKRGFASFVASNPNA P RN	
	201	250
1111FutA.pep	(196) AFYBALNSIEPVAGGGSV N TLGYN I KNKSEELSOYKENICREN O GYGY	
19C2A.pep	(16) -----	
915A.pepneose	(93) -----	
26695A.pep	(198) AFYDALNSTEPVTGGGSV N TLGYK I GNKSEELSOYKENICREN O GYGY	
1182B.pep	(197) AFYBALNSIEPVIGGGSV N TLGYN I KNKSEELSOYKENICREN O GYGY	
1218B.pep	(197) AFYBALNSIEPVIGGGSV N TLGYN I KNKSEELSOYKENICREN O GYGY	
ORF19C2B.pep	(198) AFYBALNSIEPV T GGGSV N TLGYN I KNKSEELSOYKENICREN O GYGY	
Consensus	(201) AFYDALNSIEPV GGGSV N TLGYN I KNKSEELSOYKENICREN O GYGY	

	1	50
1111FutA	(1) ATGTTCCAACCCCTATTAGATGCCTTATAGAAAGCGCT-CCATTGAAAA	
915A.cod (MWG)	(1) ATGTTCCAACCCCTATTAGATGCCTTATAGAAAGCGCTTCATTGAAAA	
19C2FutA.cod	(1) ATGTTCCAACCCCTACTAGACGCCCTTATAGAAAGCGCTTCATTGAAAA	
26695A.cod	(1) ATGTTCCAACCCCTATTAGACGCCCTTATAGAAAGCGCTTCATTGAAAA	
1182B	(1) ATGTTCCAACCCCTATTAGACGTTATATAGAAAGCGCTTCATTGAAAA	
1218B.nuc	(1) ATGTTCCAACCCCTATTAGACGTTATATAGAAAGCGCTTCATTGAAAA	
ORF19C2B	(1) ATGTTCCAACCCCTATTAGACGTTATATAGACAGCACCCGTTAGATGA	
Consensus	(1) ATGTTCCAACCCCTATTAGACGCCCTTATAGAAAGCGCTTCATTGAAAA	
	51	100
1111FutA	(50) AATGGCCTCTAAATCTCCCCCCCC-----TAAAAATCGCTGTGGCGAATT	
915A.cod (MWG)	(51) AATGGCCTCTAAATCTCCCCCCCC-----TAAAAATCGCTGTGGCGAATT	
19C2FutA.cod	(46) -----	
26695A.cod	(51) AATGGCCTCTAAATCTCCCCCCCCCCCCTAAAATCGCTGTGGCGAATT	
1182B	(51) AATTACCTCTAAATCTCCCCCCCCCCC-----TAAAAATCGCTGTGGCGAATT	
1218B.nuc	(51) AATTACCTCTAAATCTCCCCCCCCCCC-----TAAAAATCGCTGTGGCGAATT	
ORF19C2B	(51) AACCGATTATAA-----GCCCCCAT---TAAATATAGCCCTAGCGAATT	
Consensus	(51) AAT GCCTCTAAATCTCCCCCCCC TAAAAATCGCTGTGGCGAATT	
	101	150
1111FutA	(95) GGTGG-----GGAGATGA-AGAAATTAAAAATTAAAAAGAGCGTTCTT	
915A.cod (MWG)	(95) GGTGG-----GGAGATGA-AGAAATTAAAAATTAAAAAGAGCGTTCTT	
19C2FutA.cod	(46) -----	
26695A.cod	(101) GGTGG-----GGAGATGA-AGAAATTAAAAGAATTAAAAAGAGCGTTCTT	
1182B	(98) GGTGG-----GGAGATGA-AGAGGTTGAAGAATTAAAAAGAACATTCTT	
1218B.nuc	(98) GGTGG-----GGAGATGA-AGAGGTTGAAGAATTAAAAAGAACATTCTT	
ORF19C2B	(92) GGTGGCCTTGGAATAAAAGAGAAAGCAAAGGGTTAGAAAAAAATTATC	
Consensus	(101) GGTGG GGAGATGA AGAAATTAAAAGAATTAAAAAGA C TTCTT	
	151	200
1111FutA	(139) T---ATTTTATCCTAACGCCAGCATTACACAATCAGTTACACGGAAACCC	
915A.cod (MWG)	(139) T---ATTTTATCCTAACGCCAGCATTACACAATCAGTTACACGGAAACCC	
19C2FutA.cod	(46) -----	
26695A.cod	(145) T---ATTTTATCCTAACGCCAACGCTACGCCATTACACAATCAGTTACACGGAAACCC	
1182B	(142) T---ATTTTATTCTCAGTCAGCATTACACAATCAGCTCCACCAAAACCC	
1218B.nuc	(142) T---ATTTTATTCTCAGTCAGCATTACACAATCAGCTCCACCAAAACCC	
ORF19C2B	(142) TTACATTTCAAGTCAGCATTACACAATCGCTCTCACCCACCAAAACCC	
Consensus	(151) T ATTTTAT CTAAG CAGCATTACACAATCAC CTCCACC AAACCC	
	201	250
1111FutA	(186) TGATAAACCTGGGACATCGTCTTGGTAACCCCTTGGATCAGCCAGAA	
915A.cod (MWG)	(186) TGATAAACCTGGGACATCGTCTTGGTAACCCCTTGGATCAGCCAGAA	
19C2FutA.cod	(46) -----	
26695A.cod	(192) CAATGAATTTCAGATCTAGTTTAGCAATCCTCTTGGAGCGGCTAGAA	
1182B	(189) CAACGAACCCCTCCGATCTCGTCTTGGCAGTCCTATTGGATCAGCCAGAA	
1218B.nuc	(189) CAACGAACCCCTCCGATCTCGTCTTGGCAGTCCTATTGGATCAGCCAGAA	
ORF19C2B	(192) TGATAAACCTGGGACATCGTTTGGTAACCCCTTGGATCAGCCAGAA	
Consensus	(201) AT AACCT C GA TCGTCTTGG AA CC CTTGGATCAGCCAGAA	

FIG. 13 (1/6)

	251	300
1111FutA	(236) AAATCTTATCCTATCAAAACGAAAAAGGGTGTTCACACCGGTGAAAAT	
915A.cod (MWG)	(236) AAATCTTATCCTATCAAAACGAAAAAGGGTGTTCACACCGGTGAAAAT	
19C2FutA.cod	(46) -----	
26695A.cod	(242) AGATTTATCTTATCAAAACACTAAACGAGTGTTCACACCGGTGAAAAC	
1182B	(239) AAATCTTATCCTATCAAAACGAAAAAGAGTGTTCACACCGGTGAAAAC	
1218B.nuc	(239) AAATCTTATCCTATCAAAACGAAAAAGAGTGTTCACACCGGTGAAAAC	
ORF19C2B	(242) AAATCCTATCCTATCAAAACGCTAAAGGGTGTTCACACCGGTGAAAAC	
Consensus	(251) AAATCTTATCCTATCAAAACGCAAAAG GTGTTCACACCGGTGAAAAC	
	301	350
1111FutA	(286) GAAGTCCCTAACCTAACCTCTTGATTACGCCATAGGCTTT-GATGAAT	
915A.cod (MWG)	(286) GAAGTCCCTAACCTAACCTCTTGATTACGCCATAGGCTTT-GATGAAT	
19C2FutA.cod	(46) -----	
26695A.cod	(292) GAATCACCTAATTCAACCTCTTGATTACGCCATAGGCTTT-GATGAAT	
1182B	(289) GAATCGCCTAACCTCTTGATTACGCCATAGGCTTT-GATGAAT	
1218B.nuc	(289) GAATCGCCTAACCTCTTGATTACGCCATAGGCTTT-GATGAAT	
ORF19C2B	(292) GAAGTCCCTAACCTCTTGATTACGCCATAGGCTTT-GATGAAT	
Consensus	(301) GAA CCTAATTCAACCTCTTGATTACGCCATAGGCTTT GATGAAT	
	351	400
1111FutA	(335) TGGACTTTAGAGATCGTTATTCAGAATGCCTTGATTATGCCATTG	
915A.cod (MWG)	(334) -----	
19C2FutA.cod	(46) -----	
26695A.cod	(341) TGGATTTAATGATCGTTATTCAGAATGCCTTGATTATGCCATTG	
1182B	(338) TGGATTTAGAGATCGTTATTCAGAATGCCTTGATTATGATAGACTA	
1218B.nuc	(338) TGGATTTAGAGATCGTTATTCAGAATGCCTTGATTATGATAGACTA	
ORF19C2B	(341) TGGACTTTAGAGATCGTTATTCAGAATGCCTTGATTATGATAGACTA	
Consensus	(351) TGGA TTTAGAGATCGTTATTCAGAATGCCTTGATTATGATAGACTA T	
	401	450
1111FutA	(385) CATTATAAGCCGAGCTTGTAAATGACACCAACTCGCCTTATAAACTCAA	
915A.cod (MWG)	(334) -----	
19C2FutA.cod	(46) -----	
26695A.cod	(391) CACTATAAGCCGAGCTTGTAAATGACACCAACTCGCCTTACAACCTCAA	
1182B	(388) CACCATAAGCCGAGAGCGTGAATGACACCAACTCGCCTTACAACCTCAA	
1218B.nuc	(388) CACCATAAGCCGAGAGCGTGAATGACACCAACTCGCCTTACAACCTCAA	
ORF19C2B	(391) CACCATAAGCCGAGAGCGTGAATGACACCAACCGCAGCTTACAAGATTAA	
Consensus	(401) CAC ATAAAGCCGAG GT AATGACACCAACT CGCCTTACAACCTCAA	
	451	500
1111FutA	(435) ACCTGACAGCCTTATGCTTTAAAAAAACCCCTCCCATCATTTAAAGAAA	
915A.cod (MWG)	(334) -----	
19C2FutA.cod	(46) -----	
26695A.cod	(441) AGACAACAGCCTTATGCTTTAAAAAAACCCCTCTCATCATTTAAAGAAA	
1182B	(438) ACCTGACAGCCTTATGCTTTAAAAAAACCCCTCCCATCATTTAAAGAAA	
1218B.nuc	(438) ACCTGACAGCCTTATGCTTTAAAAAAACCCCTCCCATCATTTAAAGAAA	
ORF19C2B	(441) ATCTGACAGCCTTATGCTTTAAAAAAACCCCTCCCATCATTTAAAGAAA	
Consensus	(451) A CTGACAGCCTTATGCTTTAAAAAAACCCCTCCCATCATTTAAAGAAA	

FIG. 13 (2/6)

		501	550
1111FutA	(485)	ACCACCCAATTTGTGCGCAGTAGTGAATAATGAGAGTGATCCTTGAAA	
915A.cod (MWG)	(334)	-----	
19C2FutA.cod	(46)	-----	
26695A.cod	(491)	ACCACCCCTAATTTGTGCGCAGTAGTGAATGATGAGAGCGATCTTTAAAA	
1182B	(488)	ACCACCCAATTATGCGCAGTAGTGAACAATGAGAGCGATCCTTGAAA	
1218B.nuc	(488)	ACCACCCAATTATGCGCAGTAGTGAACAATGAGAGCGATCCTTGAAA	
ORF19C2B	(491)	ACCACCCACATTATGCGCGCTAACATAATGAGATCGATCCTTGAAA	
Consensus	(501)	ACCACCC AATTT TGCGCAGTAGTGAA AATGAGAGCGATCCTTGAAA	
		551	600
1111FutA	(535)	AGAGGGTTTGCAGCTTGTAGCGAGCAACGCTAACGCTCCTATGAGGAA	
915A.cod (MWG)	(334)	-----	
19C2FutA.cod	(46)	-----	
26695A.cod	(541)	AGAGGGTTTGCAGCTTGTAGCGAGCAACGCTAACGCTCCTATGAGGAA	
1182B	(538)	AGAGGGTTTGCAGCTTGTAGCGAGCAACGCTAACGCTCCTAAAGGAA	
1218B.nuc	(538)	AGAGGGTTTGCAGCTTGTAGCGAGCAACGCTAACGCTCCTAAAGGAA	
ORF19C2B	(541)	AGAGGGTTTGCAGCTTGTAGCGAGCAACGCTAACGCCCTATAAGGAA	
Consensus	(551)	AGAGGGTTTGCAGCTTGTAGCGAG TTTGT GC AGCAACGCTAACGCTCCTA AAGGAA	
		601	650
1111FutA	(585)	CGCTTTTATGAGGCTTAAACGCTATTGAGCCAGTTACTGGGGGAGGGA	
915A.cod (MWG)	(334)	-----	
19C2FutA.cod	(46)	-----	
26695A.cod	(591)	CGCTTTTATGACGCTCTAAATTCTATAGAGCCAGTTACTGGGGGAGGAA	
1182B	(588)	TGCTTTCTATGACGCTTAAATTCTATAGAGCCAGTTACTGGGGGAGGGA	
1218B.nuc	(588)	TGCTTTCTATGACGCTTAAATTCTATAGAGCCAGTTACTGGGGGAGGGA	
ORF19C2B	(591)	CGCTTTCTATGAGGCTTAAATTCTATTGAGCCAGTTACTGGGGGAGGGA	
Consensus	(601)	GCTTT TATGA GCTTAAATTCTAT GAGCCAGTTA TGGGGGAGGGA	
		651	700
1111FutA	(635)	GCGTGAAAAACACTTTAGGCTATAATGTCAAAAACAAGAGCGAGTTTTA	
915A.cod (MWG)	(334)	-----	
19C2FutA.cod	(46)	-----	
26695A.cod	(641)	GTGTGAGAAAACACTTTAGGCTATAAGGTGGAAACAAAAGCGAGTTTTA	
1182B	(638)	GCGTGAAAAACACTTTAGGCTATAACATTAACAGAGCGAGTTTTA	
1218B.nuc	(638)	GCGTGAAAAACACTTTAGGCTATAACATTAACAGAGCGAGTTTTA	
ORF19C2B	(641)	GCGTGAGAAAACACTTTAGGCTATAACGTCAAAAACAAAAGCAATTG	
Consensus	(651)	GCGTGA AAAACACTTTAGGCTATAA T AAAAACAA AGCGAGTTTTA	
		701	750
1111FutA	(685)	AGCCAATACAAATTCAATCTGTGTTTGAAAACACTCAAGGCTATGGCTA	
915A.cod (MWG)	(334)	-----	
19C2FutA.cod	(46)	-----	
26695A.cod	(691)	AGCCAATACAAGTTCAATCTCTGTGTTTGAAAACACTCGCAAGGTTATGGCTA	
1182B	(688)	AGCCAATACAATTCAATCTGTGTTTGAAAACACTCAGAGGCTATGGCTA	
1218B.nuc	(688)	AGCCAATACAATTCAATCTGTGTTTGAAAACACTCAGAGGCTATGGCTA	
ORF19C2B	(691)	AGCCAATACAAGTTCAATCTGTGTTTGAAAACACTCAAGGCTATGGCTA	
Consensus	(701)	AGCCAATACAA TTCAATCTGTGTTTGAAAAC C CAAGGCTATGGCTA	

FIG. 13 (3/6)

		751		800
1111FutA	(735)	TGTAACTGAAAAGATCATTGACGCTTATTCAGCCATACCATTCCATT		
915A.cod (MWG)	(334)	-----		
19C2FutA.cod	(46)	-----		
26695A.cod	(741)	TGTAACCGAAAAAAATCCTTGATGCGTATTTAGCCATACCATTCCATT		
1182B	(738)	TGTAACTGAAAAGATCATTGACGCTTACTTAGCCATACCATTCCATT		
1218B.nuc	(738)	TGTAACTGAAAAGATCATTGACGCTTACTTAGCCATACCATTCCATT		
ORF19C2B	(741)	TGTTACTGAAAAGATCATTGACGCTTACTCAGCCACACCATTCCATT		
Consensus	(751)	TGTAACTGAAAAGATCATTGACGCTTAAAGCCATACCATTCCATT		
		801		850
1111FutA	(785)	ATTGGGGG--AGTCC-CAGCGTGGCGAAAGATTTAACCTAACAGAGTT		
915A.cod (MWG)	(334)	-----		
19C2FutA.cod	(46)	-----		
26695A.cod	(791)	ATTGGGGG--AGTCC-CAGCGTGGCGAAAGATTTAACCTAACAGAGTT		
1182B	(788)	ATTGGGGG--AGTCC-TAGCGTGGCACAAAGATTTAACCTAACAGAGTT		
1218B.nuc	(788)	ATTGGGGG--AGTCC-TAGCGTGGCACAAAGATTTAACCTAACAGAGTT		
ORF19C2B	(791)	ATTGGGGGGAGTCCCTAGCGTGGCGAAAGATTTAACCCC-----		
Consensus	(801)	ATTGGGGG AGTCC AGCGTGGC AAGATTTAACCTAA AGTTTT		
		851		900
1111FutA	(832)	GTGAATGTCCATGATTCAACAACATTGATGAAGCGATTGACTATATCAG		
915A.cod (MWG)	(334)	-----		
19C2FutA.cod	(46)	-----		
26695A.cod	(838)	GTGAATGTGCATGATTCAACAACATTGATGAAGCGATTGATTATATCAA		
1182B	(835)	GTGAATGTTGTGATTAAAGATTGATGAAGCGATTGATCATGTGCG		
1218B.nuc	(835)	GTGAATGTTGTGATTAAAGATTGATGAAGCGATTGATCATGTGCG		
ORF19C2B	(832)	-----		
Consensus	(851)	GTGAATGT TGATT AA A TTTGATGAAGCGATTGA AT T		
		901		950
1111FutA	(882)	ATAC TTGCACACGCACCCAAACGCTTATTTAGACATGCACTATGAAAACC		
915A.cod (MWG)	(334)	-----		
19C2FutA.cod	(46)	-----		
26695A.cod	(888)	ATACCTGGACACGCACCCAAACGCTTATTTAGACATGCTCTATGAAAACC		
1182B	(885)	ATAC TTGCACACGCACCCAAACGCTTATTTAGACATGCTTATGAAAACC		
1218B.nuc	(885)	ATAC TTGCACACGCACCCAAACGCTTATTTAGACATGCTTATGAAAACC		
ORF19C2B	(832)	-----		
Consensus	(901)	ATAC TGCACACGCACCCAAACGCTTATTTAGACATGC TATGAAAACC		
		951		1000
1111FutA	(932)	CTTTAAACACTATTGATGGAAAGCTTACTTTACCAAATTTGAGTTT		
915A.cod (MWG)	(334)	-----		
19C2FutA.cod	(46)	-----		
26695A.cod	(938)	CTTTAAACACCCCTGATGGAAAGCTTACTTTACCAAATTTGAGTTT		
1182B	(935)	CTTTAAACACCCCTGATGGAAAGCTTACTTTACCAAATTTGAGTTT		
1218B.nuc	(935)	CTTTAAACACCCCTGATGGAAAGCTTACTTTACCAAATTTGAGTTT		
ORF19C2B	(832)	-----		
Consensus	(951)	CTTTAAACAC TTGATGGAAAGCTTACTTTACCAA ATTTGAGTTT		

FIG. 13 (4/6)

		1001	
1111FutA	(982)	AAAAAAATCCTAGATTTTTAAAACGATTTAGAAAACGACACCGATCTA	1050
915A.cod(MWG)	(334)	-----	
19C2FutA.cod	(46)	-----	
26695A.cod	(988)	AAAAAAATCCTAGATTTTTAAAACGATTTAGAAAACGATACGGATTTA	
1182B	(985)	AAAAAAATCCTAGATTTTTAAAACGATTTAGAAAACGACACCGATTTA	
1218B.nuc	(985)	AAAAAAATCCTAGATTTTTAAAACGATCTAGAAAACGACACCGATTTA	
ORF19C2B	(832)	-----	
Consensus	(1001)	AAAAAAATCCTAGATTTTTAAAACGAT TTAGAAAACGA ACGAT TA	
		1051	
1111FutA	(1032)	TCACGATAACCC-----TTTCATTTCTATCGTATTGAATGAGCCTT	1100
915A.cod(MWG)	(334)	-----	
19C2FutA.cod	(46)	-----	
26695A.cod	(1038)	TCACAAATTCTCAACATCTTCATGTGGGAGTACGATCTGCATAAGCCGT	
1182B	(1035)	TCACGATAACCC-----TTTTATTTTTATCGTATTGAATGAGCCTT	
1218B.nuc	(1035)	TCACGATAACCC-----TTTTATTTTTATCGTATTGAATGAGCCTT	
ORF19C2B	(832)	-----	
Consensus	(1051)	TCAC A C C TTT AT T A GAT TG AT AGCC T	
		1101	
1111FutA	(1076)	CAGTATCTATTGATGGT---TTGAGGGTTAACATTATGATGATTGAGGGTT	1150
915A.cod(MWG)	(334)	-----	
19C2FutA.cod	(46)	-----	
26695A.cod	(1088)	TAGTATCCATTGATGAT---TTGAGGGTTAACATTATGATGATTGAGGGTT	
1182B	(1079)	TAATATCTATTGATGATGATTGAGGGTTAACATTATGATGATTGAGGGTT	
1218B.nuc	(1079)	TAATATCTATTGATGAT---TTGAGGGTTAACATTATGATGATTGAGGGTT	
ORF19C2B	(832)	-----	
Consensus	(1101)	A TATC ATTGATG T TTGAGGGTTAACATTATGATGATTGAGGGTT	
		1151	
1111FutA	(1123)	AATTATGATGATTGAGGGTTAACATTATGATGATTGAGGGTTAACATTATGA	1200
915A.cod(MWG)	(334)	-----	
19C2FutA.cod	(46)	-----	
26695A.cod	(1135)	AATTATGACCGGCTTTACAAAACGCCCTCGCCTTATTAGAACTCTCTCA	
1182B	(1129)	AATTATGATGATTGAGGGTTAACATTATGATGATGATTGAGGGTTAACATTATGA	
1218B.nuc	(1126)	AATTATGATGATTGAGGGTTAACATTATGATGATGATTGAGGGTTAACATTATGA	
ORF19C2B	(832)	-----	
Consensus	(1151)	AATTATGA T AA T TTT G T T A	
		1201	
1111FutA	(1173)	GCGCCTTTACAAAACGCCCTCGCCTTATTAGAACTCTCTCAAAACACCA	1250
915A.cod(MWG)	(334)	-----	
19C2FutA.cod	(46)	-----	
26695A.cod	(1185)	AAACACCACTTTAAAATCTATCGCAAAGCTTATCAAAATCCTGCCTT	
1182B	(1179)	TGATTTGAGGGTTAACATTATGATGATTGAGGGTTAACATTATGATGATTGA	
1218B.nuc	(1176)	TGATTTGAGGGTTAACATTATGATGATTGAGGGTTAACATTATGATGATTGA	
ORF19C2B	(832)	-----	
Consensus	(1201)	AA	

FIG. 13 (5/6)

		1251		
1111FutA	(1223)	CTTTAAAATCTATCGCAAAGCTTATCAAAAATCCTTGCCTTGTTGCGT		1300
915A.cod (MWG)	(334)	-----		
19C2FutA.cod	(46)	-----		
26695A.cod	(1235)	TGTTGCGCGCGGTGAGAAAGTTGGTTAAAAAATTGGGTTTGTA-----		
1182B	(1229)	GGGTTAATTATGATGATTGAGGGTTAATTATGATGATTGAGGGTTAAT		
1218B.nuc	(1226)	GGGTTAATTATGATGATTGAGGGTTAATTATGATGATTGAGGGTTAAT		
ORF19C2B	(832)	-----		
Consensus	(1251)	T	T A A	
		1301		1350
1111FutA	(1273)	GCCATAAGGAGATGGGTTAAAAAGTAA-----		
915A.cod (MWG)	(334)	-----		
19C2FutA.cod	(46)	-----		
26695A.cod	(1279)	-----		
1182B	(1279)	TATGATGATTGAGGGTTAATTATGATGATTGAGGGTTAATTATGAGCG		
1218B.nuc	(1276)	TGTGATGATTGAGGGTTAATTATGATGATTGAGGGTTAATTATGAGCG		
ORF19C2B	(832)	-----		
Consensus	(1301)			
		1351		1400
1111FutA	(1300)	-----		
915A.cod (MWG)	(334)	-----		
19C2FutA.cod	(46)	-----		
26695A.cod	(1279)	-----		
1182B	(1329)	GCTCTTACAAAACGCCCTCGCCTTATTAGAACCTCTCAAAACACCACTT		
1218B.nuc	(1326)	GCTCTTACAAAACGCCCTCGCCTTATTAGAACCTCTCAAAACACCACTT		
ORF19C2B	(832)	-----		
Consensus	(1351)			
		1401		1450
1111FutA	(1300)	-----		
915A.cod (MWG)	(334)	-----		
19C2FutA.cod	(46)	-----		
26695A.cod	(1279)	-----		
1182B	(1379)	TTAAAATCTATCGCAAAGCTTATCAAAAATCCTTACCTTGTTGCGTGC		
1218B.nuc	(1376)	TTAAAATCTATCGCAAAGCTTATCAAAAATCCTTACCTTGTTGCGTGC		
ORF19C2B	(832)	-----		
Consensus	(1401)			
		1451		1483
1111FutA	(1300)	-----		
915A.cod (MWG)	(334)	-----		
19C2FutA.cod	(46)	-----		
26695A.cod	(1279)	-----		
1182B	(1429)	GCGAGAAAGTTGATTAAAAATTGGGTTTGTA		
1218B.nuc	(1426)	GCGAGAAAGTTGATTAAAAATTGGGTTTGTA		
ORF19C2B	(832)	-----		
Consensus	(1451)			

FIG. 13 (6/6)

Oligo Structures

Lacto-N-neo-Tetraose (LNnT)

Gal β 1-4GlcNAc β 1-3Gal β 1-4Glc

Lacto-N-Fucopentaose III (LNFP III)

Gal β 1-4GlcNAc β 1-3Gal β 1-4Glc

3

|

1 α Fucose

FIG. 14

Linkage Analysis by GC/MS

The samples were methylated, hydrolyzed, reduced with sodium borodeuteride, acetylated and analyzed by GC/MS along with samples of LNNT and LNF3.

- A Glc vs. Glc-NAc value close to 1 favors fucosylation of Glc-NAc.
- A Glc vs. Glc-NAc value close to 0 favors fucosylation of Glc

<i>H. Pylori</i> Strain	Glc vs. Glc-NAc
915A2	0.982
19C2A5	0.040
1111A2	0.975
19C2B1	0.991
1182B3	0.983

FIG. 15

1 Liter LNFIII Synthesis

Batch Number	Resin Type	Total Yield	Actual Percent Recovery
1-02	MR3 NH_4HCO_3 column (1ml resin/1ml synthesis)	1.567 g	61%
2-02	MR3 NH_4HCO_3 column (1ml resin/1ml synthesis)	1.760 g	68%
3-02	Dowex1/Dowex 50 (2ml resin/1ml synthesis)	1.221 g	47%

FIG. 16

FIG. 17

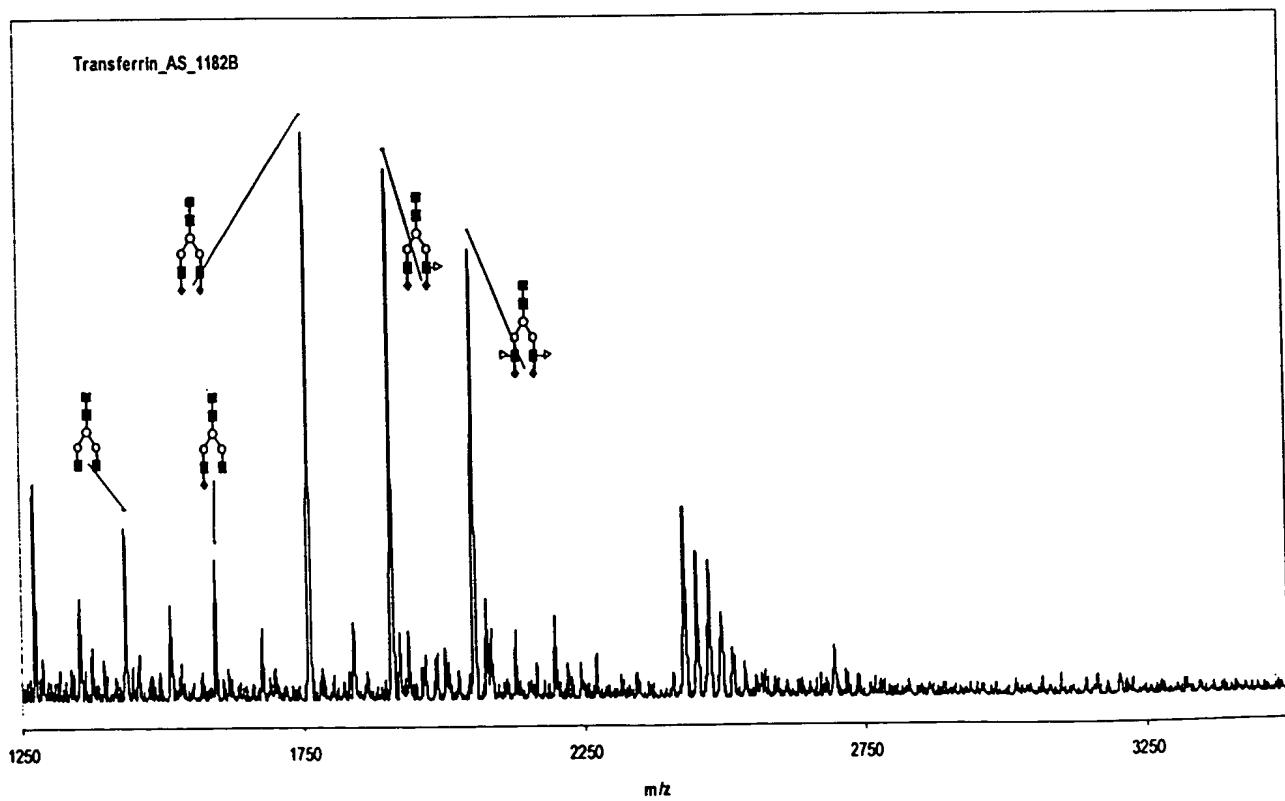
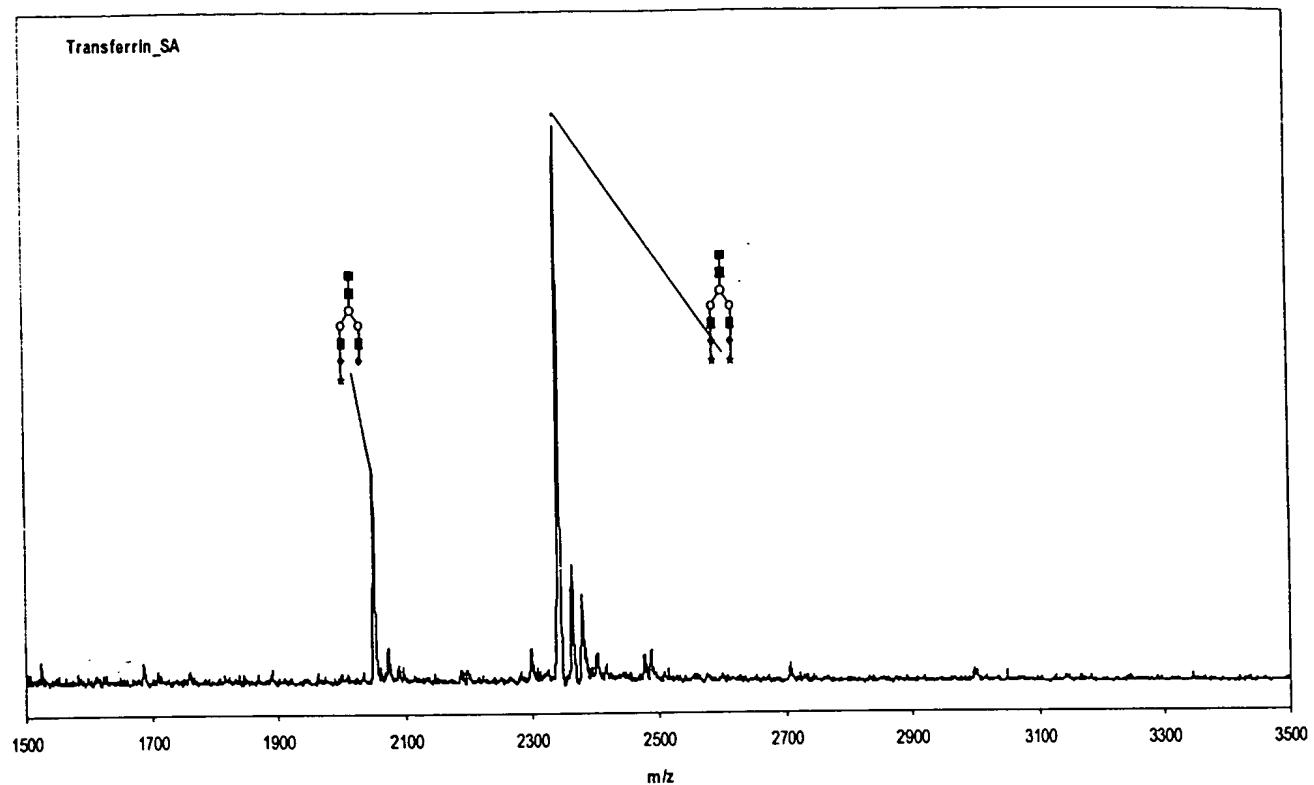


FIGURE 18

Strain 1111FutB fucosyltransferase nucleotide coding sequence (SEQ ID NO:15)

ggatccCGAGCGACCAATCATTACAGGGATTATTGCATTAGATGCCGCTTCAGTAACACGCTGATCGTGGAAAATAACGCCTTAAACGGCTTGGTTACCGGGCATATGATGTTTACATTCTAAAGGGCAAATGCTCC TCGCTTGCAACGCTCGTTGAATATCAGTAAAGATCGCACTTAGTCGTGGCGATGGGGCAATGATTG AGCATGTTAACACATGCCCATATTAAAATCGCTTCAACGCTAAAGAGGTTTAAAACAGCACGCCACGCA TTGCATCAATGACCTAATCTAGCCCTAATCAAGCCTTGTAAAAATTTCCTGTTGATGTTACAAAATTTTTGTAACATTCCCT TTAAAAGGATAGCCatgttccaacccctattagacgcttagttagaaagcgcttcattgaaaaaatggcc tctaaatctccccccccctaaaatcgctgtggcgaattgggtggggagatgaagaaattaaagaattaa aaagagcggttttatcttttagccaacgcacacaatgcctccaccaaaaccccaatgaatttt cagatctagtcttagcaatcccttgatcagctagaaaaatcttgcataaaacgcctaaagagtg tttcacccggtaaaatgaagtccctaacttcaacctcttgcattacgccttaggcattgtatgaaatttgc ttttagagatcgttatttgcggatgccttataattatgcattttgcacaccataaagccgagagcgtgaatg acaccacttcgcctacaaactcaaagacaacgccttatactttaaaaaaccccccataattaaa gaaaaccaccctaatttagcgcagtcgtgaatgtgagagcgatccttggaaaagaggggtgtgagctt gtagcgagcaacgcataacgcctcatgagaaacgcctttatgcgtttaattctattgagccagttac tgggggagggagcgtgaaaacactttaggctataacgtcaaaaacaagagcgagtttaagccaataca agttcaacctgtgtttgaaaactcacaaggctatggctatgttaaccgagaagatccttgcgccttacttt agcccacaccattctatttattgggggagtcctagcgtggcgaagatttaaacctttaaagagttgtgaa tgcattgtttcaacaacttgcattgtgaagcgatagattatataaaatacttgcacacgcacccaaacgcctt atttagacatgcctatgaaaaccctttaacgccttgcattttggaaagcttactttaccaggatttgagt ttaaaaaaaaatcctagctttttaaaacgattttgaaaacgcatacgatttacaaaatcctcaacatc tttcatgtggagtgcgtctcgatgagccgttagcgtctattgtgatttgagggttaattatgtatgattt gagggtaattatgtgatttgagggttaattatgtgatttgagggttaattatgtgatttgagggtta attatgtgatttgagggttaattatgcgccttgcaaaacgccttacccatttggaaattatccaaa acacctttttaaatctatgccaaaggctatcaaaggctatcaaaaatccttacccttattgcgcgcattt aaGGAGATGGGTTAAAAGTAAGGTGCTTTAAAGACTGGGTGAGAAATTGAAGCGCTATTAAAATGCG CTAACCGCTTCTTTTGAGCGTGGGGTTTGAGCATGTCCTCTAAAGCATGGCGCTTAAAATGTTTG GATTTAAAGACACGATGCCCAAAGGATTCTCTTAGAAAGGTTAAAAGGCGTTGGGCAAAATCTC GCCAAATACGATAATGACTTTGAAGCGCTGTTGCTAATTGCCAGGTCGgaattc

Strain 1111FutB fucosyltransferase amino acid sequence (SEQ ID NO:16)

MFQPLLDAYVESASIEKMASKSPPPLKIAVANWWGDEEIKEFKKSVLYFISQRYTIALHQNPNEFSDLVF
SNPLGSARKILSYQNAKRVFTGENEVPNFNLFDYAIGFDELDFRDRYLRMPLYYDRLHHKAESVNDTSP
YKLKDNSLYTLKKPSHQFKENHPNLCAVVNDESPLKRGVVSVNASANAPMRNAFYDALNSIEPVTTGGGS
VKNTLGYNVKNKSEFLSQYKFNLCFENSQGYGYVTEKILDAYFSHTIPIYWGPSVAKDFNPKEFVNVDHF
NNFDEAIDYIKYLHTHPNAYLDMYLENPLNALDGKAYFYQDLSFKKILAFFKTILENDTIYHKSSTSFMWE
CDLDEPLASIDDLRVNYDDLRLVNYDDLRLVNYDDLRLVNYDDLRLVNYERLLQNASPILLELSQNTSF
KIYRKAYQKPIKNPYPYCAP

FIGURE 19

Strain 802FutA fucosyltransferase nucleotide coding sequence (SEQ ID NO:17)

ggatccCGGCGTGAATTACTACCTTCTGGCTTGACAGCTATGCCGAGGCATCCCTGCCTATCCCTA
CTTCTTATACTTTGGTAGCGATACTTGTCTCGTATTGGCTATTCAAACGCCATTGAGT
TTGCCCTAAATTGGTTAAAGGATAGCCTGTTCCAGCCCTACTAGACGCCCTTATAGAAAGTGCCTCAAT
TAAAAAAATGCCCTGTAGTTACCCCCCTAAAATGCCGTGGGAATTGGTGGGGAGGCGCTGAAGAAT
TTAAAAGAGCGCTATGTATTCTAACGCTACACAATCACCCACCAAAACCCCAACGAA
CCCTCCGATCTGTCTTGGCAGTCCTATTGGAGCAGCAGAAAATCCTATCCTACCAAAACACTAAAAG
AGTGTGTTACGCCGGTAAAATGAAGTCCCTAATTCAACCTTTGATTACGCCATAGGCTTGATGAAT
TGGATTTAGAGATCGTTATTGAGAATGCCCTTATATTGATAGACTACACCATAAGCCGAGAGCGTG
AATGACACCACCGCGCCTACAAGATTAACCTGACAGCCTTATACCTTAAAAAACCTCCCATTCAATT
TAAAGAAAAACACCCCCATTATGCGCAGTAGTGAATGATGAGAGCGATCCTTGAAGAGGGTTGCGA
GTTTGTGCAAGCAACCTAACGCTCTAAAAGGAACGCCCTATGACGCTTAAATTCTATTGAGCCA
GTTACTGGGGGAGGGAGCGTGAACACTTTAGGCTATAAGTGGAAACAAAACGAGTTTTAAGCCA
ATACAAATTCAATCTGTGTTTGAACACTCTCAAGGCTATGGCTATGTAACGAAAAAATCATTGACGCTT
ACTTTAGCCATACCATTCTATTGAGGGAGTCCTAGCGTGGCAAAGATTAAACCTAAGAGTTT
GTGAATGTGATGATTAAAACCTTGTGAAGCGATTGATTACGTGAGATACTTGACACGCACCCAAA
CGCTTATTTAGACATGCTCTATGAAACCCCTTAAACACCCCTGATGGAAAGCTTACTTTACCAAGATT
TGAGTTTAAAAAAATCCTAGATTGAGGTTAGATTGAGAGCGATTATAATAATT
GAGAGCCGATTATAATAATTGAGAGCCGATTATAATAATTGAGAGCCGATTATAATAATTGAGAGCCG
ATTACGATGCCGTTACAAACCGTTGCCCTTGGAACTCTCTAAACACCCACTTTAAATCTAT
CACAAAGCTTATCACAATCCTAACCTTGTGCGTGCATAAGGAGATGGGTTAAAAAATGGGTTGta
aATTGGGGTAATCAAACCCCTGCGTACATCGCAGACGCCACTTTCTAAACCAAGCGATATTAGCC
CCTAAACAAATTAGTAGGGCTTAAACTCTTTAGGGTTGAGAGACATTAAATCTCTTCA
GATGTGGTGTAAATTCCGATCCACCACTTCAAAACTCCAAGGGTGCATGCTCGCTTGCCTGCGCATTCCA
AGCCGCTCACGCTACCCCCCAGCATTAGCCGCTGCCTACCAAGAAATCTAGCCTGAAAAAC
AATTCAATCGCTTATTGCTGAGGGCATGTTGCCCCCTCAGCCACGCATTGCACCCATTAGAAAGGAG
GGTTTGCggattc

Strain 802FutA fucosyltransferase amino acid sequence (SEQ ID NO:18)

MFQPLLDLAFIESASIKMPLSYPLKIAVANWWGAEFFKSAMYFILSQRYTITLHQNPNEPSDLVFGSP
IGAARKILSYQNTKRVFYAGENEVPNFNLFDYAI GFDELDLDRYLRMPLYYDRLHHKAESVNDDTAPYKI
KPDSLYTLKKPSHHFKEKPHLCAVNDESPLKRGFASFVASNPNA PKRNAFYDALNSIEPV TGGGSVKN
TLGYKVGKNEFLSQYKFNLCFENSQGYGYTEKIIDAYFSHTIPIYWGPSVAKDFNPKSFVNVDHFKNF
DEAIDYVRLHTPNAYLDMLYENPLNLTLDGKAYFYQDLSFKKILDFFKTILENDTIYHNNPFVFYRDLNE
PLVSIDDLRADYNNLRADYNNLRADYNNLRADYNNLRADYDRLLQNRSPLLELSQNTTFK IYHKAYHKSLP
LLRAIRRWVKLGL

FIGURE 20

Strain 948FutA fucosyltransferase nucleotide coding sequence (SEQ ID NO:19)

Strain 948FutA fucosyltransferase amino acid sequence (SEQ ID NO:20)

MQPPLDAFIDSTHLDDETTKPPLNVALANWWPLKNSEKKGFRDFILHFILKQRYKIILHSNPNEPSDLVF
GNPLEQARKILSYQNTKRVFTYGENEVPNFLFDYAIGFDELFNDRMLPLYAYLHYKAMLVNDTSP
YKLKALYTLKKPSHKFKENHPNLCALIHNESDPWKRGFASFASNPNAPIRNAFYDALNAIEPVASGGSVK
NTLGYKVKNKNEFLSQYKFNLCFENSQGYGYVTEKILDAYFSHTIPIYWGPSVAKDFNPKSFVNVDFFNN
FDEAIDYIRYLHAHQNAYLDMLYENPLNTIDGKAGFYQDLSFEKILDFFKNILENDTIYHCNDAHYSALHR
DLNEPLVSDDLRRDHDDLRVNYDDLRLRVNYDDLRLVNYDDLRRDHDDLRDHERLLSK
ATPLLELSQNTSFKIYRKAYQKSLPLLRAI

FIGURE 21

Strain 955FutA fucosyltransferase nucleotide coding sequence (SEQ ID NO:21)

ggatccGAGCACCATTACAGGGATTATTAAATTAGATGTGCTTCAGTAACACGCTGATAAGT
GGAAAATGGTGCCTTAAACGGCTTGGTTACGGGCATATGATGTTTCAACTCTAAAGGC
GAAATGCTTCAGCCCTACAACGCTTGCTAAATATCAGTGAAACGAGCA
TTAGTTGCTGGCGATGGAGCGAATGACTTG
AGCatgtTCAAACATGCCATTAAATCGCTTCAACGCTAAAGAGGTTTAAA
ACAACAGGCCAGCA
TTGCATCAATGAGCCTGATTAGCCCTAACAGCCTTGATTAAAAAATTTTTG
TAAAGGATAAAGATGTTCCAGCCCCATTAGATGCTTCATAGAAAGC
GCTTCAATTAAAGGAGCTCTAACTC
CTCTAAATCTCCCCCCCCCTAAACACGCTGTGGCGAATTGGTTAACGG
ACTAAAGAATTAAAGCGAG
CGTCTTTATTCATCTAAACACGCTATAAAATCATTCTGCACAGCA
ACCCCTAATGAACCCCTCAGATC
TAGTCTTGGCAATCCTTGGAAACAAGCCAGAAAAATCTTATCTT
ACCGGGGAAATGAAGTGCCTAATTCAATCTCTTGTATTAGCC
TATTAGCCATTATAAGCCATGCTTGTAAATGACACCA
CGATCGCTATTGAGAATGCTTGTATTAGCCATTATAAGCCATGCTTGTAA
CTTCGCCTATAAACTCAAAGCCTTTACTTTAAAAACCTTCC
CATAAAATTAAAGAAAACCACCC
AATTATGTGCGCTAACCATACGAGAGCGATCCTGGAAAAGAGGG
TTGCCAGTTTGTGCAAGCTAGGGAG
TCCTAACGCTCCCATCAGAAACGCTTCTATGACGCTTAAATG
CTATTGAGCCAGTGGCTAGTGGAG
GTGTGAAAACACTCTAGGCTATAAGGTC
AAAAACAAAACGAATT
TTAAGCCAATACAAGTCAACCTC
TGTTTGAAAACCTACAAGGCTATGGCTATGTAACG
AAAAAATTCC
TGATGCGTATTCA
GCCCCACACTA
TCCCTATTATTGGGGGAGTCCAGCGTGGCGAAAGATT
TAACCTAAAGTTGATG
CTTCAACAACTTGTGATGAAGCGATTGATTATCAG
ATTACACGCC
ACCAAAACGCTATTAGACAT
GCTTTATGAAAACCC
CTTAAACACCATTGATGG
GAGCGGGTTTACCAAG
ATTGAGTTGAGTTGAAAAGA
TCTTAGATT
TTTCAAAACATTCTGAAA
ACGATACGATT
TATCATTGCAATGATGCC
ATTACTCTGCT
CTTCATCGTATTG
GAATGAGCGTTAGTGTCT
GTGATGATTGAGAAGAG
GATCATGATGATTGAGGGT
TAATTATGATGATTG
GAGAAGAG
GATCATGAA
ACGCC
CTTAAAGGCT
ACCC
CTTACCC
TTGCGTGC
CATAAGGAAG
TGGGTT
AAAAAATAAGCGT
ATT
TTAAGACTG
ATGAGAA
ATTGAGCG
CTATT
TTAAAG
TGC
GCTAA
ACGCC
TTCT
TTTGAGCGT
GGGGTTT
TTGAGC
ATGT
CCTCTAA
AGC
ATGG
GTCT
AAAAAATG
TTGTT
TTAAG
ACG
CGT
CCAA
AGG
ATT
CTTCT
TTAG
AAAGG
TTAAA
AGG
CGTT
GGG
CAA
ATCT
CGCC
AA
AT
ACC
ACA
ATG
ACT
TTT
GAAG
CGT
GTT
GCT
AA
TGT
GCC
AGG
TCG
Gga
attc

Strain 955FutA fucosyltransferase amino acid sequence (SEQ ID NO:22)

MFKHAHIKIAFNAKEVLQHQATHCINEPDALALIKPLIFKIFFVKYSFKG. RCSSPY. MPS. KALQLKKNCL
ISPLPKIAVANWFNGTKEFKASVLYFILKQRYKIIILHSNPNEPSDLVFGNPLEQARKILSYQNTKRVFYT
GENEVPNFLFDYAI GFDELD FNDRYL RMLP YYAYLHYKAMLVNDTTSPYKLKALYTLKKPSHKFKENHPN
LCALIHNESDPWKRGFASFVASNPNAPIRNAFYDALNAIEPVASGGSVKNTLGYKVKNKNEFLSQYKFNL
FENSQGYGYVTEKIP. CVFQPHYPYLLGESQRGERF. P. KFCECA. FQQL. SD. LYQIFTRAPKRLFRHA
L. KPLKHH. WESGFLPRFEF. KDLRFFQKHS. KRYDLSLQ. CPLFCSSS. FE. AVSVC. FEKRS. FEG.
L. FEKRS. TPLIKGYPSTGAIPKHLE. NLSQSLSKVLTUVACHKEVG. KIRRII RLMMKKLKRYFKMR. RF
FFERGVFEHVL. SMGA. KMFCF. RHDAKGFFF RKV. KA FGQNLAKYHND. SAVV. LPGRN

FIGURE 22

Strain 1218FutA fucosyltransferase nucleotide coding sequence (SEQ ID NO:23)

ggatccTCTGGCTTGACAGCTATGCCGAGGCATCCCTGCCTATCCCTACTTTCTTATACTTTGG
TAGCGATACCTTCGCTCTCGTGTCTGGCTATTCAAACGCCATTGAGTTGCCTAAATTGGTTAA
AGGATAACCAGTCCAACCCCTATTAGCCTTATAGAAAAGCGCTTCAATTGAAAAAATTACCTCTAA
ATCTCCCCCCCCCTAAAAATCGCTGGCGAATTGGTGGGGAGATGAAGAGGTTGAAGAATTAAAAAGA
ACATTCTTATTATTCTCAGTCAGCATTACACAATCACCCCTCCACCAAAACCCAAACGAACCCCTCGAT
CTCGTCTTGGCAGTCCTATTGGATCAGCCAGAAAAATCTTATCCTATCAAACGCCAAAGAGTGTGTTA
CACCGGTGAAAAGGAATGCCATTCAACCTCTTGATTACGCCATAGGCTTGATGAATGGATTAG
AGATCGTTATTAAGAATGCCTTATATTGATAGACTACACCATAAAGCCGAGAGCGTGAATGACACCA
CTTCGCCTTACAAACTCAAACCTGACAGCCTTATGCTTAAAAACCCCTCCCATATTAAAGAAAAC
CACCCCAATTATGCGCAGTAGTGAACAATGAGAGCGATCCCTTGAAGAGGGTTGCGAGTTGTAGC
GAGCAACCTAACGCTCCTAAAAGGAATGCTTCTATGACGCTTAAATTCTATAGAGCCAGTTATTGGGG
GAGGGAGCGTGAACACTTAGGCTATAACATTAAAACAAGAGCGAGTTTAAGCCAATACAAATT
AACTGTGTTTGAACACTCACAAGGCTATGGCTATGTAAGTGAACAACTTACATTGACGCTTACTTTAGCA
TACCATCCATTATTATTGGGGAGTCCTAGCGTGGCACAAGATTAAACCTAAGAGTTGTGAATGTT
GTGATTAAAGATTGATGAAGCGATTGATCATGTGCGATACTTGACACGCCCCAACGCTTATT
GACATGTTATGAAAACCTTAAACACCCTGATGGAAAGCTTACTTTCCAAAATTGAGTTTAAAA
AAATCCTAGATTAAACGATCTAGAAAACGACACGATTATCACGATAACCCTTATTGAGTTT
CGTGATTGAATGAGCGTTAATATCTATTGATGATTGAGGGTTAATTATGATGATTGAGGGTTAATT
TGATGATTGAGGGTTAATTATGATGATTGAGGGTTAATTATGATGATTGAGGGTTAATTATGATGATT
TGAGGGTTAATTATGATGATTGAGGGTTAATTATGATGATTGAGGGTTAATTATGATGATTGAGGGTT
AATTGTGATGATTGAGGGTTAATTATGATGATTGAGGGTTAATTATGAGCGCTTACAAAACGCTC
GCCTTATTAGAACCTCTCAAAACACCACCTTAAATCTATCGCAAAGCTTATCAAAACCTTACCTT
TGTTGCGTGGCGAGAAAGTTGATTAAAAAATTGGTTGTAAATTGGGGTAATCAAAACCCCTTGC
TATCATCGCAGGCCACCTTCTAAACACCAGCGATATTAGCCCCTAAACAAAATTAGTAGGGTCTTAA
ACTCTTAGCGGTTTGAGAGACATTCTTATAAgaattc

Strain 1218FutA fucosyltransferase amino acid sequence (SEQ ID NO:24)

MFQPLLDAYIESASIEKITSKSPPPLKIAVANWWGDEEVEEFKKNILYFILSQHYTITLHQNPNEPSDLVF
GSPIGSARKILSYQNAKRVFYTGENSEPNFNLFDYAI GFDEWILEIVI . ECLYIMIDYTIKPRA . MTPLRL
TNSNLTAFML . KNPPII LKKTTPIYAQ . TMRAIL . KEGLRVL . RATLTLLKGMLSMTL . IL . SQLLGEGA
. KTL . AITLKTRASF . ANTSICVLKTHKAMAM . LKKSLTTLAIPFLFIGGVLAWHKILTLRVL . MFVIL
KILMKRLIMCDTCTRTQTLI . TCFMKT . TPLMGKLTQNLFSKKILDFFKTILENDTIYHDNPFI FYRDL
NEPLISIDDLRVNYDDL RVNYDDL RVNYDDL RVNYDDL RVNYDDL RVNYDDL RVNYDDL RVNC
DLRVNYDDL RVNYERLLQNASPLLELSQNTTFKIYRKAYQKSLPLLRAARKLIK LG . NWG . SNPLRYHR
RRHLSKTS DISP . NKISRVFKLFSGLRDILIRIRYQAYRYRRPRGGAR